

#2



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,156

DATE: 03/19/2002^{8.5}

TIME: 16:22:30

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J086156.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
 BETA-SUBUNITS,
 6 K+betaM4 and K+betaM5
 8 <130> FILE REFERENCE: D0115NP
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/086,156
 C--> 10 <141> CURRENT FILING DATE: 2002-02-28
 10 <150> PRIOR APPLICATION NUMBER: US 60/272,190
 11 <151> PRIOR FILING DATE: 2001-02-28
 13 <150> PRIOR APPLICATION NUMBER: US 60/274,258
 14 <151> PRIOR FILING DATE: 2001-03-07
 16 <160> NUMBER OF SEQ ID NOS: 98
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1839
 22 <212> TYPE: DNA
 23 <213> ORGANISM: homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (5)..(1057)
 29 <400> SEQUENCE: 1
 30 acaa atg acc ggg agc cat gac gtc atc ggg ggc gca gga aag cag gtg 49
 31 Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val
 32 1 5 10 15
 34 ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca 97
 35 Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro
 36 20 25 30
 38 ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat 145
 39 Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn
 40 35 40 45
 42 gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg 193
 43 Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val
 44 50 55 60
 46 acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc 241
 47 Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys
 48 65 70 75
 50 cgt gaa gga cta ctt cca gca acc cag tct cct gcc atg tcc gac ccc 289
 51 Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro
 52 80 85 90 95
 54 atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc 337
 55 Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr
 56 100 105 110
 58 ctg acc agc ttc cct gac tcc atg cta ggc gcc atg ttc agc ggg aag 385
 59 Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys

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60	115	120	125	
62	atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac	433		
63	Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp			
64	130	135	140	
66	ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt	481		
67	Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu			
68	145	150	155	
70	gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc	529		
71	Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala			
72	160	165	170	175
74	gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa	577		
75	Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu			
76	180	185	190	
78	gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg	625		
79	Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu			
80	195	200	205	
82	aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag	673		
83	Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln			
84	210	215	220	
86	atc tac agc ctc tcc tct tcc agc atg gag gtc ttc aac gcc aac atc	721		
87	Ile Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile			
88	225	230	235	
90	ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tct aag ctc ttc	769		
91	Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe			
92	240	245	250	255
94	tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac	817		
95	Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp			
96	260	265	270	
98	ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca	865		
99	Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro			
100	275	280	285	
102	gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc	913		
103	Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro			
104	290	295	300	
106	gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg	961		
107	Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu			
108	305	310	315	
110	aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat	1009		
111	Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His			
112	320	325	330	335
114	gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg	1057		
115	Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg			
116	340	345	350	
118	taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc	1117		
120	ttggagggca tctcgccagt ggtgcgaggc aggggactat actaatctgt attaatgtg	1177		
122	tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa	1237		
124	cagaaccacc ttttttcttg ccatttttgag ctgcagacag gcggtttatt atgacaagt	1297		
126	aagagtcagc tgatgtgtac taaaggaggc cataggagga ttttccagcc aggacaaaag	1357		
128	agcagcagtt ttctcctggg ctccatctct ctgtaccgct agccagtgcc gcatttatcc	1417		

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```

130 atctgtaaga aggccctggt ggagaggatg ggatgagaac aagaggctac ctccaggttaa 1477
132 ccaggacata aagtccccag cggttcctgt cacacctgct cctccctccc caggggtgcat 1537
134 ccatgatcgt ggatgtttgc ccaggggtga ccatgttttg ctggcttgga atgctgtgca 1597
136 ttctcagagc tctgttagtg tccccctctg ggggtcagag atgaggtgtg gcaggggtcta 1657
138 gaggaatgag tgtccaggca gagttcagaa ggtaggaatg tccctcttga tagggctgaa 1717
140 tcaagggatt cctggcttta gaaaggtct gctatctttg caaaaatgtg caagtatctg 1777
142 tagccagtgt aatgaaatca ctccaaaatc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1837
144 aa 1839

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147 <210> SEQ ID NO: 2

148 <211> LENGTH: 351

149 <212> TYPE: PRT

150 <213> ORGANISM: homo sapiens

152 <400> SEQUENCE: 2

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154 Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val Leu
155 1 5 10 15
158 Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
159 20 25 30
162 Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn Ala
163 35 40 45
166 Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val Thr
167 50 55 60
170 His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys Arg
171 65 70 75 80
174 Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile
175 85 90 95
178 Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu
179 100 105 110
182 Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met
183 115 120 125
186 Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly
187 130 135 140
190 Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp
191 145 150 155 160
194 Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp
195 165 170 175
198 Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val
199 180 185 190
202 Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn
203 195 200 205
206 Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
207 210 215 220
210 Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe
211 225 230 235 240
214 Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr
215 245 250 255
218 Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro
219 260 265 270
222 Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu
223 275 280 285

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```

226 Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala
227      290      295      300
230 Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys
231 305      310      315      320
234 Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala
235      325      330      335
238 Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
239      340      345      350
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 237
244 <212> TYPE: PRT
245 <213> ORGANISM: homo sapiens
247 <400> SEQUENCE: 3
249 Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
250 1      5      10      15
252 Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
253      20      25      30
255 Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
256      35      40      45
258 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
259      50      55      60
261 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
262 65      70      75      80
264 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
265      85      90      95
267 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
268      100      105      110
270 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
271      115      120      125
273 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
274      130      135      140
276 Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
277 145      150      155      160
279 Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
280      165      170      175
282 Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
283      180      185      190
285 His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
286      195      200      205
288 Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
289      210      215      220
291 Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
292 225      230      235
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 256
296 <212> TYPE: PRT
297 <213> ORGANISM: homo sapiens
299 <220> FEATURE:
300 <221> NAME/KEY: UNSURE

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301 <222> LOCATION: (15)..(15)

302 <223> OTHER INFORMATION: wherein "X" is equal to any amino acid.

305 <400> SEQUENCE: 4

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W--> 307 Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
308 1 5 10 15
310 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
311 20 25 30
313 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
314 35 40 45
316 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
317 50 55 60
319 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
320 65 70 75 80
322 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
323 85 90 95
325 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
326 100 105 110
328 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
329 115 120 125
331 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
332 130 135 140
334 Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
335 145 150 155 160
337 Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
338 165 170 175
340 Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
341 180 185 190
343 Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
344 195 200 205
346 Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
347 210 215 220
349 Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
350 225 230 235 240
352 Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
353 245 250 255
355 <210> SEQ ID NO: 5
356 <211> LENGTH: 234
357 <212> TYPE: PRT
358 <213> ORGANISM: homo sapiens
360 <400> SEQUENCE: 5
362 Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His
363 1 5 10 15
365 Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu
366 20 25 30
368 Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro
369 35 40 45
371 Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser
372 50 55 60
374 His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

DATE: 03/19/2002

PATENT APPLICATION: US/10/086,156

TIME: 16:22:31

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J086156.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8